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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/660,302C

DATE: 07/31/2002 P.6
TIME: 10:05:17

Input Set : A:\EP.txt

Output Set: N:\CRF3\07312002\I660302C.raw

1 <110> APPLICANT: Universiteit Utrecht
2 Strous, Gerardus
3 Van Kerkhof, Petrus
4 Govers, Roland
6 <120> TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF
PROTEASE
7 INHIBITORS OR RECEPTOR FRAGMENTS
9 <130> FILE REFERENCE: 2183-4525US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/660,302C
12 <141> CURRENT FILING DATE: 2000-09-12
14 <150> PRIOR APPLICATION NUMBER: PCT/NL99/00136
15 <151> PRIOR FILING DATE: 1999-03-12
17 <150> PRIOR APPLICATION NUMBER: EP98200799.9
18 <151> PRIOR FILING DATE: 1998-03-12
20 <160> NUMBER OF SEQ ID NOS: 50
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 8
26 <212> TYPE: PRT
27 <213> ORGANISM: Unknown
29 <220> FEATURE:
30 <221> NAME/KEY: BINDING
31 <222> LOCATION: (1)..(8)
32 <223> OTHER INFORMATION: synthetic peptide, Binding polypeptide motif
34 <220> FEATURE:
35 <221> NAME/KEY: UNSURE
36 <222> LOCATION: (1)..(1)
37 <223> OTHER INFORMATION: Xaa may be any amino acid
39 <220> FEATURE:
40 <221> NAME/KEY: UNSURE
41 <222> LOCATION: (2)..(2)
42 <223> OTHER INFORMATION: Xaa is E, but may be replaced by D
44 <220> FEATURE:
45 <221> NAME/KEY: UNSURE
46 <222> LOCATION: (3)..(3)
47 <223> OTHER INFORMATION: Xaa is F, but may be replaced by Y
49 <220> FEATURE:
50 <221> NAME/KEY: UNSURE
51 <222> LOCATION: (4)..(4)
52 <223> OTHER INFORMATION: Xaa is I, but may be replaced by L, V or F
54 <220> FEATURE:
55 <221> NAME/KEY: UNSURE
56 <222> LOCATION: (5)..(5)
57 <223> OTHER INFORMATION: Xaa may be any amino acid

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59 <220> FEATURE:
60 <221> NAME/KEY: UNSURE
61 <222> LOCATION: (6)..(6)
62 <223> OTHER INFORMATION: Xaa may be any amino acid
64 <220> FEATURE:
65 <221> NAME/KEY: UNSURE
66 <222> LOCATION: (7)..(7)
67 <223> OTHER INFORMATION: Xaa is D, but may be replaced by E
69 <220> FEATURE:
70 <221> NAME/KEY: UNSURE
71 <222> LOCATION: (8)..(8)
72 <223> OTHER INFORMATION: Xaa may be any amino acid
74 <400> SEQUENCE: 1
W--> 75 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
76 1 5
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 12
80 <212> TYPE: PRT
81 <213> ORGANISM: Unknown
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Unsure, Growth hormone receptor binding motif, Binds to
hormone receptor
85 and ubiquitin
87 <400> SEQUENCE: 2
88 Asp Asp Ser Trp Val Glu Phe Ile Glu Leu Asp Ile
89 1 5 10
91 <210> SEQ ID NO: 3
92 <211> LENGTH: 10
93 <212> TYPE: PRT
94 <213> ORGANISM: Unknown
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Unsure, Growth hormone receptor motif, Binds to hormone
receptor and
98 ubiquitin
100 <400> SEQUENCE: 3
101 Asp Ser Trp Val Glu Phe Ile Glu Leu Asp
102 1 5 10
104 <210> SEQ ID NO: 4
105 <211> LENGTH: 129
106 <212> TYPE: PRT
107 <213> ORGANISM: Unknown
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Unsure, Growth hormone receptor motif, Up-regulates GH
activity
112 <400> SEQUENCE: 4
113 Ser Lys Gln Gln Arg Ile Lys Met Leu Ile Leu Pro Pro Val Pro Val
114 1 5 10 15
115 Pro Lys Ile Lys Gly Ile Asp Pro Asp Leu Leu Lys Glu Gly Lys Leu
116 20 25 30
117 Glu Glu Val Asn Thr Ile Leu Ala Ile His Asp Ser Tyr Lys Pro Glu
118 35 40 45
119 Phe His Ser Asp Asp Ser Trp Val Glu Phe Ile Glu Leu Asp Ile Asp

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```

120      50      55      60
121 Glu Pro Asp Glu Lys Thr Glu Glu Ser Asp Thr Asp Leu Leu Ser Ser
122 65      70      75      80
123 Asp His Glu Lys Ser His Ser Asn Leu Gly Val Lys Asp Gly Asp Ser
124      85      90      95
125 Gly Arg Thr Ser Cys Cys Glu Pro Asp Ile Leu Glu Thr Asp Phe Asn
126      100      105      110
127 Ala Asn Asp Ile His Glu Gly Thr Ser Glu Val Ala Gln Pro Gln Arg
128      115      120      125

```

129 Leu

131 <210> SEQ ID NO: 5

132 <211> LENGTH: 38

133 <212> TYPE: PRT

134 <213> ORGANISM: Unknown

136 <220> FEATURE:

137 <223> OTHER INFORMATION: Unsure, Derived from protein receptor, Up-regulates GH
activity

139 <400> SEQUENCE: 5

140 Lys Asp Gly Asp Ser Gly Arg Thr Ser Cys Cys Glu Pro Asp Ile Leu

141 1 5 10 15

142 Glu Thr Asp Phe Asn Ala Asn Phe Ile His Glu Gly Thr Ser Glu Val

143 20 25 30

144 Ala Gln Pro Gln Arg Leu

145 35

147 <210> SEQ ID NO: 6

148 <211> LENGTH: 10

149 <212> TYPE: PRT

150 <213> ORGANISM: Unknown

152 <220> FEATURE:

153 <223> OTHER INFORMATION: Unsure, Glut4 Ins-regulated glucose transporter binding
motif, Binds to

154 ubiquitin/proteasome system binding site

156 <400> SEQUENCE: 6

157 Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu

158 1 5 10

160 <210> SEQ ID NO: 7

161 <211> LENGTH: 7

162 <212> TYPE: PRT

163 <213> ORGANISM: Unknown

165 <220> FEATURE:

166 <223> OTHER INFORMATION: Unsure, Binding poly-peptide motif, Binds to
ubiquitin/proteasome system

167 binding site

169 <400> SEQUENCE: 7

170 Cys Glu Glu Asp Phe Tyr Arg

171 1 5

173 <210> SEQ ID NO: 8

174 <211> LENGTH: 10

175 <212> TYPE: PRT

176 <213> ORGANISM: Homo sapiens (human) or Lepus unknown species (rabbit)

178 <220> FEATURE:

179 <223> OTHER INFORMATION: GHR sequence

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Input Set : A:\EP.txt

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```

181 <400> SEQUENCE: 8
182 Ser Trp Val Glu Phe Ile Glu Leu Asp Ile
183 1 5 10
185 <210> SEQ ID NO: 9
186 <211> LENGTH: 10
187 <212> TYPE: PRT
188 <213> ORGANISM: Gallus gallus (chicken)
190 <220> FEATURE:
191 <223> OTHER INFORMATION: GHR
193 <400> SEQUENCE: 9
194 Leu Trp Val Glu Phe Ile Glu Leu Asp Ile
195 1 5 10
197 <210> SEQ ID NO: 10
198 <211> LENGTH: 10
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens (human)
202 <220> FEATURE:
203 <223> OTHER INFORMATION: prolactin receptor
205 <400> SEQUENCE: 10
206 Leu Leu Val Glu Tyr Leu Glu Val Asp Asp
207 1 5 10
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 10
211 <212> TYPE: PRT
212 <213> ORGANISM: Mus musculus (mouse), Lepus unknown species (rabbit), or Rattus
unknown
W--> 213 species (rat)
215 <220> FEATURE:
216 <223> OTHER INFORMATION: prolactin receptor
218 <400> SEQUENCE: 11
219 Leu Leu Val Glu Phe Leu Glu Asn Asp Asp
220 1 5 10
222 <210> SEQ ID NO: 12
223 <211> LENGTH: 10
224 <212> TYPE: PRT
225 <213> ORGANISM: Unknown
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Unsure, vertebrate skeletal muscle
230 <400> SEQUENCE: 12
231 Asp Asn Val Asp Tyr Leu Thr Arg Asp Trp
232 1 5 10
234 <210> SEQ ID NO: 13
235 <211> LENGTH: 10
236 <212> TYPE: PRT
237 <213> ORGANISM: Unknown
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Unsure, FGF Receptor Family
242 <400> SEQUENCE: 13
243 Gln Ala Ala Glu Tyr Leu Arg Ser Glu Thr
244 1 5 10

```

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Input Set : A:\EP.txt

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246 <210> SEQ ID NO: 14
247 <211> LENGTH: 10
248 <212> TYPE: PRT
249 <213> ORGANISM: Unknown
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Unsure, Transmembrane receptor sex precursor
254 <400> SEQUENCE: 14
255 Ile Asp Ala Glu Tyr Ile Ser Ala Glu Arg
256 1 5 10
258 <210> SEQ ID NO: 15
259 <211> LENGTH: 10
260 <212> TYPE: PRT
261 <213> ORGANISM: Unknown
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Unsure, IgE Receptor
266 <400> SEQUENCE: 15
267 Leu Lys Gly Glu Phe Ile Trp Val Asp Gly
268 1 5 10
270 <210> SEQ ID NO: 16
271 <211> LENGTH: 10
272 <212> TYPE: PRT
273 <213> ORGANISM: Unknown
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Unsure, ANGIOTENSIN CONVERTING ENZYME
278 <400> SEQUENCE: 16
279 Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly
280 1 5 10
282 <210> SEQ ID NO: 17
283 <211> LENGTH: 10
284 <212> TYPE: PRT
285 <213> ORGANISM: Unknown
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Unsure, POTASSIUM CHANNEL IRK
290 <400> SEQUENCE: 17
291 Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln
292 1 5 10
294 <210> SEQ ID NO: 18
295 <211> LENGTH: 10
296 <212> TYPE: PRT
297 <213> ORGANISM: Unknown
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Unsure, PDGF RECEPTOR ALPHA-CHAIN
302 <400> SEQUENCE: 18
303 Asp Gly His Glu Tyr Ile Tyr Val Asp Pro
304 1 5 10
306 <210> SEQ ID NO: 19
307 <211> LENGTH: 10
308 <212> TYPE: PRT
309 <213> ORGANISM: Unknown

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/660,302C

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,3,4,5,6,7,8

Seq#:50; Xaa Pos. 4

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 84

Seq#:7; Line(s) 166

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:213 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:322 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0